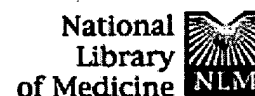


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#55 Search #54 AND fusion		11:36:22	<u>8</u>
#54 Related Articles for PubMed (Select 8322511)		11:33:59	<u>157</u>
#52 Search pir2 hsp150		10:53:27	<u>6</u>
#45 Search #42 AND yeast		10:46:55	<u>26</u>
#42 Related Articles for PubMed (Select 9023548)		10:40:07	<u>109</u>
#40 Search l-selectin yeast		10:39:38	<u>17</u>
#39 Search l-selectin		10:39:26	<u>2608</u>
#38 Search matilla glycobiology		10:39:13	<u>0</u>
#37 Search matilla targeting		10:39:03	<u>0</u>
#36 Search matilla fusion		10:38:45	<u>0</u>
#35 Search matilla lewis		10:38:31	<u>0</u>
#34 Search matilla yeast		10:38:08	<u>3</u>
#9 Related Articles for PubMed (Select 12626410)		08:50:33	<u>104</u>
#32 Search #30 AND pir		08:45:49	<u>3</u>
#30 Related Articles for PubMed (Select 12766345)		08:45:18	<u>95</u>
#28 Search zueco fusion		08:40:51	<u>5</u>
#27 Search jaafar fusion		08:40:40	<u>1</u>
#26 Search moukadiri fusion		08:40:29	<u>1</u>
#25 Search pir1 fusion		08:13:49	<u>4</u>
#24 Search jigami and pir		08:09:50	<u>2</u>
#23 Search shimma and pir		08:09:39	<u>2</u>
#22 Search yoh-ichi and pir		08:09:14	<u>0</u>
#21 Search ohba and pir		08:08:48	<u>2</u>
#20 Search abe and pir		08:08:36	<u>3</u>
#18 Search #17 AND pir		08:07:11	<u>9</u>
#17 Related Articles for PubMed (Select 10438739)		08:06:53	<u>103</u>
#16 Search #9 AND pir		08:06:39	<u>6</u>
#7 Search #6 and pir		08:00:37	<u>12</u>
#6 Related Articles for PubMed (Select 14734022)		08:00:08	<u>94</u>
#2 Search #1 AND fusion		07:59:42	<u>46</u>
#1 Search pir		07:53:08	<u>976</u>

(FILE 'HOME' ENTERED AT 13:10:57 ON 11 FEB 2004)

FILE 'REGISTRY' ENTERED AT 13:11:39 ON 11 FEB 2004

L1 13 S PIR1

FILE 'MEDLINE, AGRICOLA, CAPLUS, BIOSIS, EMBASE, WPIDS' ENTERED AT  
13:12:00 ON 11 FEB 2004

L2 2 S L1 AND FUSION

L3 6 S L1 AND (CELL (W) WALL)

L4 5 DUP REM L3 (1 DUPLICATE REMOVED)

FILE 'STNGUIDE' ENTERED AT 13:14:26 ON 11 FEB 2004

FILE 'MEDLINE, AGRICOLA, CAPLUS, BIOSIS, EMBASE, WPIDS' ENTERED AT  
13:19:09 ON 11 FEB 2004

L5 93 S (PIR1? OR PIR2? OR PIR3? OR PIR4?) AND (YEAST OR CEREVISIAE)

L6 60 S L5 AND (FUSION OR (CELL (W) WALL))

L7 19 DUP REM L6 (41 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 13:21:23 ON 11 FEB 2004

FILE 'CAPLUS' ENTERED AT 13:23:55 ON 11 FEB 2004

E ABE HIR/AU 25

L8 3 S (E19 OR E20) AND (PIR1? OR PIR2? OR PIR3? OR PIR4? OR PIR!)

E SHIMMA YOH/AU 25

L9 3 S (E4 OR E5 OR E6) AND (PIR1? OR PIR2? OR PIR3? OR PIR4? OR PIR

E JIGAMI YO/AU 25

L10 3 S (E4 OR E5) AND (PIR1? OR PIR2? OR PIR3? OR PIR4? OR PIR!)

=>

## RESULT 1

YSCPIR1P

LOCUS YSCPIR1P 1400 bp DNA linear PLN 03-FEB-1999

DEFINITION S. cerevisiae Pirlp gene.

ACCESSION D13740

VERSION D13740.1 GI:218456

KEYWORDS Pirlp.

SOURCE Saccharomyces cerevisiae (baker's yeast)

ORGANISM Saccharomyces cerevisiae

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

REFERENCE 1 (bases 1 to 1400)

AUTHORS Toh-e,A., Yasunaga,S., Nisogi,H., Tanaka,K., Oguchi,T. and  
Matsui,Y.TITLE Three yeast genes, PIR1, PIR2 and PIR3, containing internal tandem  
repeats, are related to each other, and PIR1 and PIR2 are required  
for tolerance to heat shock

JOURNAL Yeast 9 (5), 481-494 (1993)

MEDLINE 93311116

PUBMED 8322511

REFERENCE 2 (bases 1 to 1400)

AUTHORS Toh-e,A.

TITLE Direct Submission

JOURNAL Submitted (20-NOV-1992) Akio Toh-e, University of Tokyo, Department  
of Biology; 7-3-1 Hongo, Bunkyo-ku, Tokyo 113, Japan  
(E-mail:toh-e@uts2.s.u-tokyo.ac.jp, Tel:03-3812-2111(ex.4465),  
Fax:03-5684-9420)

COMMENT Submitted (20-Nov-1992) to DDBJ by:

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University of Tokyo

7-3-1 Hongo

Tokyo 113

Japan

Phone: 03-3812-2111 x4465

Fax: 03-5684-9420.

FEATURES Location/Qualifiers

source

1. .1400

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/mol\_type="genomic DNA"

/db\_xref="taxon:4932"

gene

139. .1164

/gene="PIR1"

CDS

139. .1164

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/codon\_start=1

/product="Pirlp"

/protein\_id="BAA02885.1"

/db\_xref="GI:218457"

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A A V S Q I G D G Q I Q A T T K T T S A K T T A A A V S Q I G D G Q I Q A T T K T K A A A V S Q I G D G Q I Q A T T  
K T T A A A V S Q I G D G Q I Q A T T K T T A A A V S Q I G D G Q I Q A T T N T T V A P V S Q I T D G Q I Q A T T L  
T S A T I I P S P A P A P I T N G T D P V T A E T C K S S G T L E M N L K G G I L T D G K G R I G S I V A N R Q F Q  
F D G P P P Q A G A I Y A A G W S I T P E G N L A I G D Q D T F Y Q C L S G N F Y N L Y D E H I G T Q C N A V H L Q  
A I D L L N C"

BASE COUNT 415 a 350 c 221 g 414 t

# ORIGIN

## Alignment Scores:

Pred. No.:	6.15e-92	Length:	1400
Score:	1708.00	Matches:	341
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-09-989-975-1 (1-341) x YSCPIR1P (1-1400)

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Qy	21	AlaProLysAspProTrpSerThrLeuThrProSerAlaThrTyrLysGlyGlyIleThr	40
Db	199	GCTCCAAAGGACCCGTGGTCCACTTTAACTCCATCAGCTACTTACAAGGGTGGTATAACT	258
Qy	41	AspTyrSerSerThrPheGlyIleAlaValGluProIleAlaThrThrAlaSerSerLys	60
Db	259	GATTACTCTTCTACTTTTCGGTATTGCTGTTGAACCAATTGCCACTACTGCTTCCTCCAAG	318
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Qy	201	ThrValAlaProValSerGlnIleThrAspGlyGlnIleGlnAlaThrThrLeuThrSer	220
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Qy	261		AspGlyLysGlyArgIleGlySerIleValAlaAsnArgGlnPheGlnPheAspGlyPro	280
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Qy	281		ProProGlnAlaGlyAlaIleTyrAlaAlaGlyTrpSerIleThrProGluGlyAsnLeu	300
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Db	1099		GATGAGCACATTGGAACCTCAATGTAATGCAGTCCACCTACAAGCTATCGATTTGCTCAAC	1158
Qy	341		Cys 341	
Db	1159		TGT 1161	